AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1-20. (canceled).

21. (new) A method of determining a risk for glaucoma in a subject, comprising

(a) assaying for at least two polynucleotide variations in a sample polynucleotide obtained from a subject, where said sample polynucleotide comprises the polynucleotide sequence set forth in SEQ ID NO:1, and wherein said at least two variations are selected from the group consisting of a variation at position 194, a variation at position 199, a variation at position 324, a variation at position 1051, a variation at position 1084, a variation at position 1627, a variation at position 1685, a variation at position 1756, a variation at position 1853, a variation at position 2830, a variation at position 3371, a variation at position 4037, and a variation at position 4346, and

(b) determining said risk based on detection of said at least two polynucleotide variations in said sample polynucleotide, wherein the presence of said at least two variations in said sample polynucleotide correlates with an elevated risk for glaucoma in a subject.

22. (new) The method according to claim 21, wherein one of said at least two polynucleotide variations is selected from the group consisting of the variation at position 4037, and the variation at position 4346.

23. (new) The method according to claim 22, wherein another of said at least two polynucleotide variations is selected from the group consisting of the variation at position 194, the variation at position 199, the variation at position 324, the variation at position 1051, the variation at position 1084, the variation at position 1627, the variation at position 1685, the variation at position 1756, the variation at position 1853, the variation at position 2830, and the variation at position 3371.

24. (new) The method according to claim 22, wherein another of said at least two polynucleotide variations is selected from the group consisting of the variation at position 194,

the variation at position 1051, the variation at position 1084, the variation at position 1627, the variation at position 1685, the variation at position 1756, and the variation at position 1853.

25. (new) The method according to claim 22, wherein another of said at least two polynucleotide variations is selected from the group consisting of the variation at position 194, the variation at position 1084, the variation at position 1627.

26. (new) The method according to claim 22, wherein one of said at least two polynucleotide variations is the variation at position 4037.

27. (new) The method according to claim 22, wherein one of said at least two polynucleotide variations is the variation at position 4346.

28. (new) The method according to claim 21, wherein one of said at least two polynucleotide variations is the variation at position 4037, and another of said at least two polynucleotide variations is the variation at position 4346.

29. (new) The method according to claim 21, wherein each of said at least two polynucleotide variations is independently selected from the group consisting of a nucleotide base substitution, a nucleotide base deletion, and a nucleotide base insertion.

30. (new) The method according to claim 21, wherein the variation at position 4037 is a G-to-A substitution.

31. (new) The method according to claim 21, wherein the variation at position 4346 is a G-to-A substitution.

32. (new) The method according to claim 21, wherein the variation at position 194 is a C-to-A substitution, the variation at position 199 is a A-to-C substitution, the variation at position 324 is a G-to-A substitution, the variation at position 1051 is a C-to-T substitution, the variation at position 1084 is a C-to-T substitution, the variation at position 1627 is a T-to-C substitution, the variation at position 1685 is a T-to-C substitution, the variation at position 1756 is a C-to-T substitution, the variation at position 1853 is a G-to-C substitution, the variation at position 2830 is a G-to-A substitution, the variation at position 3371 is a A-to-G substitution, the variation at position 4037 is a G-to-A substitution, and the variation at position 4346 is a G-to-A substitution.

33. (new) The method according to claim 28, wherein the variation at position 4037 is a G-to-A substitution and the variation at position 4346 is a G-to-A substitution.

34. (new) The method according to claim 21, wherein said assaying further comprises assaying for a third polynucleotide variation in the polynucleotide of SEQ ID NO:1, wherein said third polynucleotide variation is selected from the group consisting of a variation at position 194, a variation at position 199, a variation at position 324, a variation at position 1051, a variation at position 1084, a variation at position 1627, a variation at position 1685, a variation at position 1756, a variation at position 1853, a variation at position 2830, a variation at position 3371, a variation at position 4037, and a variation at position 4346.

35. (new) The method according to claim 21, wherein said glaucoma is primary open-angle glaucoma, or normal tension glaucoma, or both.

36. (new) The method according to claim 21, wherein the polynucleotide variations are assayed using an oligonucleotide that hybridizes with a portion of SEQ ID NO:1.

37. (new) The method according to claim 21, wherein said assaying comprises:

(a) amplifying the sample polynucleotide sequence using at least one oligonucleotide primer selected from the group consisting of:

i) an oligonucleotide primer selected from the group consisting of the oligonucleotide primers set forth in SEQ ID NOs:2 to 27,

ii) an oligonucleotide primer fully complementary to an oligonucleotide primer of i),

iii) an oligonucleotide primer that hybridizes under stringent conditions with an oligonucleotide primer of i) or ii), and

iv) an oligonucleotide primer having 60% or more identity with an oligonucleotide primer of i), iii) or iii), so as to obtain an amplification product; and

(b) sequencing the amplification product of (a).